deletions, substitutions or additions at positions except for the 455th position;

(ct) a polynucleotide containing the sequence which spans from the 441st to the 455th position of Sequence ID No. 1;

(dt) a polynucleotide containing the sequence which spans from the 449th to the 459th position of Sequence ID No. 1; and

(et) a complementary strand of the polynucleotide selected from the group consisting of (at), (bt), (ct) and (dt).

19. The polynucleotide of Claim 18, which comprises (at).

20. The polynucleotide of Claim 18, which comprises (bt).

21. The polynucleotide of Claim 18, which comprises (ct).

22. The polynucleotide of Claim 18, which comprises (dt).

23. The polynucleotide of Claim 18, which comprises (et).

24. The polynucleotide of Claim 18, further comprising at least one additional polynucleotide connected to said polynucleotide, the additional polynucleotide being selected from the group consisting of a promoter, an enhancer, an upstream activation sequence, a silencers, a upstream suppression sequence, an attenuator, a poly A tail, a nucleus transport signal, Kozak sequence, ISRE, a drug resistance factor, a gene of signal peptide, a gene of transmembrane domein, a gene of marker protein, a gene of interferon-responding protein, and a gene of interferon-non-responding protein.

25. A polynucleotide suitable for predicting the efficacy of interferon therapy using interferon-α and/or interferon-β for treating an individual who suffers from hepatitis C virus, comprising a polynucleotide selected from the group consisting of:

(ag) the polynucleotide of Sequence ID No. 2 in the sequence listing;

(bg) a modified polynucleotide derived from (ag) by inclusion of one or several

deletions, substitutions or additions at positions except for the 455th position;

(cg) a polynucleotide containing the sequence which spans from the 441st to the 455th position of Sequence ID No. 2;

(dg) a polynucleotide containing the sequence which spans from the 449th to the 459th position of Sequence ID No. 2; and

(eg) a complementary strand of the poly nucleotide selected from the group consisting of (ag), (bg), (cg) and (dg).

26. The polynucleotide of Claim 25, which comprises (ag).

27. The polynucleotide of Claim 25, which comprises (bg).

28. The polynucleotide of Claim 25, which comprises (cg).

29. The polynucleotide of Claim 25, which comprises (dg).

30. The polynucleotide of Claim 25, which comprises (eg).

31. The polynucleotide of Claim 25, further comprising at least one additional polynucleotide connected to said polynucleotide, the additional polynucleotide being selected from the group consisting of a promoter, an enhancer, an upstream activation sequence, a silencers, a upstream suppression sequence, an attenuator, a poly A tail, a nucleus transport signal, Kozak sequence, ISRE, a drug resistance factor, a gene of signal peptide, a gene of transmembrane domein, a gene of marker protein, a gene of interferon-responding protein, and a gene of interferon-non-responding protein.

32. A polynucleotide suitable for predicting the efficacy of interferon therapy using interferon-α and/or interferon-β for treating an individual who suffers from hepatitis C virus, comprising a polynucleotide selected from the group consisting of:

(aa) the polynucleotide of Sequence ID No. 3 in the sequence listing;

(ba) a modified polynucleotide derived from (aa) by inclusion of one or several

deletions, substitutions or additions at positions except for the 455th position;

(ca) a polynucleotide containing the sequence which spans from the 441st to the 455th position of Sequence ID No. 3;

(da) a polynucleotide containing the sequence which spans from the 449th to the 459th position of Sequence ID No. 3; and

(ea) a complementary strand of the polynucleotide selected from the group consisting of (aa), (ba), (ca) and (da).

33. The polynucleotide of Claim 32, which comprises (aa).

34. The polynucleotide of Claim 32, which comprises (ba).

35. The polynucleotide of Claim 32, which comprises (ca).

36. The polynucleotide of Claim 32, which comprises (da).

37. The polynucleotide of Claim 32, which comprises (ea).

38. The polynucleotide of Claim 32, further comprising at least one additional polynucleotide connected to said polynucleotide, the additional polynucleotide being selected from the group consisting of a promoter, an enhancer, an upstream activation sequence, a silencers, a upstream suppression sequence, an attenuator, a poly A tail, a nucleus transport signal, Kozak sequence, ISRE, a drug resistance factor, a gene of signal peptide, a gene of transmembrane domein, a gene of marker protein, a gene of interferon-responding protein, and a gene of interferon-non-responding protein.

39. A polynucleotide suitable for predicting the efficacy of interferon therapy using interferon-α and/or interferon-β for treating an individual who suffers from hepatitis C virus, comprising a polynucleotide selected from the group consisting of:

(ac) the polynucleotide of Sequence ID No. 4 in the sequence listing;

(bc) a modified polynucleotide derived from (ac) by inclusion of one or several

deletions, substitutions or additions at positions except for the 455th position;

(cc) a polynucleotide containing the sequence which spans from the 441st to the 455th position of Sequence ID No. 4;

(dc) a polynucleotide containing the sequence which spans from the 449th to the 459th position of Sequence ID No. 4; and

(ec) a complementary strand of the polynucleotide selected from the group consisting of (ac), (bc), (cc) and (dc) mentioned above.

40. The polynucleotide of Claim 39, which comprises (ac).

41. The polynucleotide of Claim 39, which comprises (bc).

42. The polynucleotide of Claim 39, which comprises (cc).

43. The polynucleotide of Claim 39, which comprises (dc).

44. The polynucleotide of Claim 39, which comprises (ec).

45. The polynucleotide of Claim 39, further comprising at least one additional polynucleotide connected to said polynucleotide, the additional polynucleotide being selected from the group consisting of a promoter, an enhancer, an upstream activation sequence, a silencers, a upstream suppression sequence, an attenuator, a poly A tail, a nucleus transport signal, Kozak sequence, ISRE, a drug resistance factor, a gene of signal peptide, a gene of transmembrane domein, a gene of marker protein, a gene of interferon-responding protein, and a gene of interferon-non-responding protein.

46. A vector comprising the polynucleotide of Claim 18.

47. A vector comprising the polynucleotide of Claim 25.

48. A vector comprising the polynucleotide of Claim 32.

49. A vector comprising the polynucleotide of Claim 39.

50. A method for predicting the efficacy of interferon therapy using interferon-α

and/or interferon-β for treating an individual who suffers from hepatitis C virus, comprising:

1) taking a sample containing a polynucleotide which includes at least one interferon-stimulated response element from the individual; and

2) determining whether the sample contains the polynucleotide of Claim 18, and

3a) predicting that the interferon therapy will be successful for said individual if the sample contains the polynucleotide of Claim 18 or

3b) predicting that the interferon therapy will not be successful for said individual if the sample does not contain the polynucleotide of Claim 18.

51. A method for predicting the efficacy of interferon therapy using interferon-α and/or interferon-β for treating an individual who suffers from hepatitis C virus, comprising:

1) taking a sample containing a polynucleotide which includes at least one interferon-stimulated response element from the individual; and

2) determining whether the sample contains the polynucleotide of Claim 25, and

3a) predicting that the interferon therapy will be successful for said individual if the sample contains the polynucleotide of Claim 25 or

3b) predicting that the interferon therapy will not be successful for said individual if the sample does not contain the polynucleotide of Claim 25.

52. A method for predicting the efficacy of interferon therapy using interferon-α and/or interferon-β for treating an individual who suffers from hepatitis C virus, comprising:

1) taking a sample containing a polynucleotide which includes at least one interferon-stimulated response element from the individual; and

2) determining whether the sample contains the polynucleotide of Claim 32, and

3a) predicting that the interferon therapy will be successful for said individual if the sample contains the polynucleotide of Claim 32 or

3b) predicting that the interferon therapy will not be successful for said individual if the sample does not contain the polynucleotide of Claim 32.

53. A method for predicting the efficacy of interferon therapy using interferon-α and/or interferon-β for treating an individual who suffers from hepatitis C virus, comprising:

1) taking a sample containing a polynucleotide which includes at least one interferon-stimulated response element from the individual; and

2) determining whether the sample contains the polynucleotide of Claim 39, and

3a) predicting that the interferon therapy will be successful for said individual if the sample contains the polynucleotide of Claim 39 or

3b) predicting that the interferon therapy will not be successful for said individual if the sample does not contain the polynucleotide of Claim 39.

54. A method for rendering an interferon-insensitive individual to be interferon-sensitive, which comprises introducing the polynucleotide of Claim 18 into the interferon-insensitive individual.

55. A method for rendering an interferon-insensitive individual to be interferon-sensitive, which comprises introducing the polynucleotide of Claim 25 into the interferon-insensitive individual.

56. A method for rendering an interferon-insensitive individual to be interferon-sensitive, which comprises introducing the polynucleotide of Claim 32 into the interferon-insensitive individual.

57. A method for rendering an interferon-insensitive individual to be interferon-sensitive, which comprises introducing the polynucleotide of Claim 39 into the interferon-insensitive individual.

58. A non-human transgenic animal, into which has been introduced the